

Supplementary Material

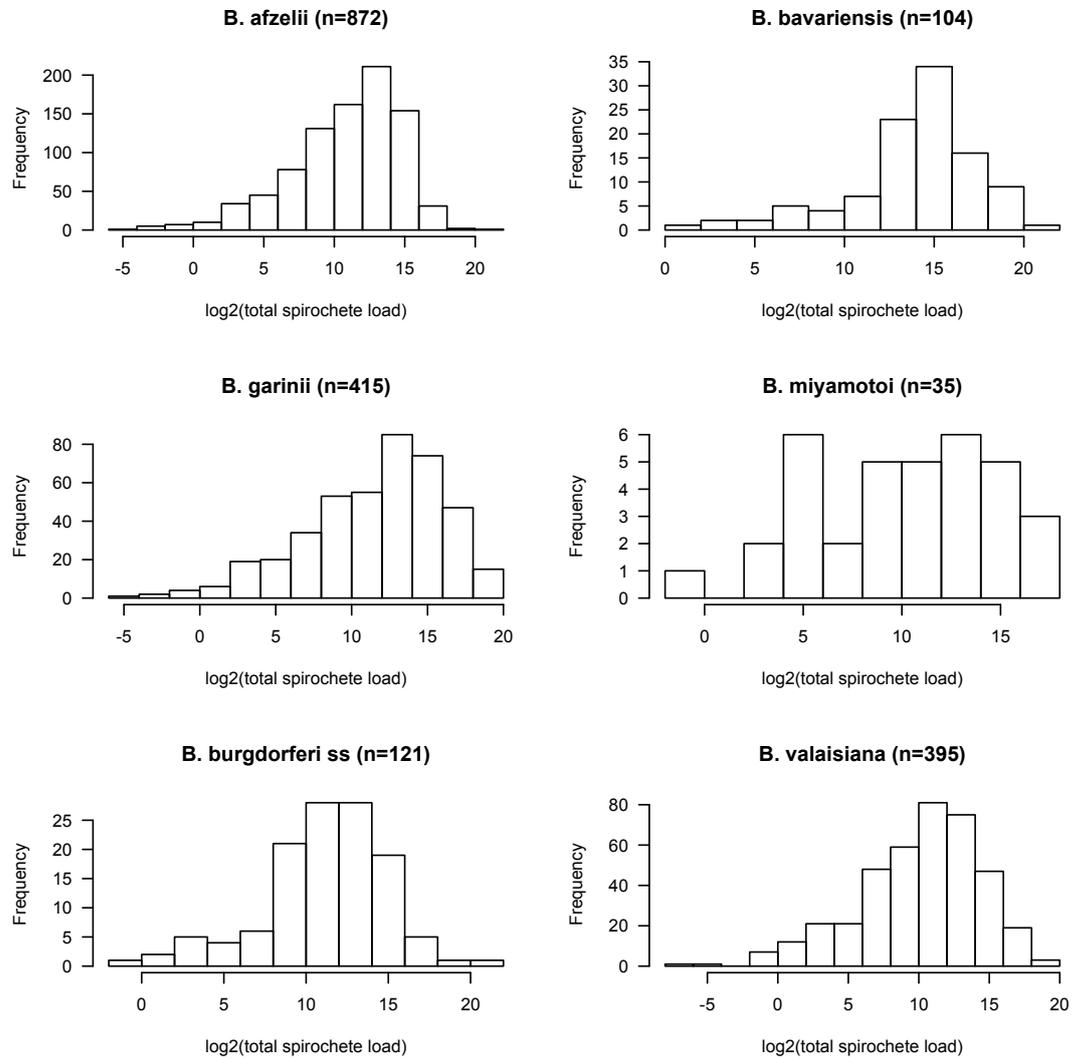


Figure S1. The log₂-transformed spirochete loads for each of the six *Borrelia* genospecies. Each distribution contains the spirochete loads for the single and double infections of that particular genospecies.

Table S1. The prevalences of the single and double infections for each of the six *Borrelia* genospecies for each of the seven sampling occasions (A-G).

study	species1	species2	infection	nymph.tot	nymph.inf	% inf
A	af	af	single	500	71	14.2
A	af	bav	double	500	0	0.0
A	af	ga	double	500	0	0.0
A	af	miy	double	500	2	0.4
A	af	ss	double	500	2	0.4
A	af	vs	double	500	0	0.0
A	bav	bav	single	500	6	1.2
A	bav	ga	double	500	0	0.0
A	bav	miy	double	500	0	0.0
A	bav	ss	double	500	0	0.0
A	bav	vs	double	500	0	0.0
A	ga	ga	single	500	13	2.6
A	ga	miy	double	500	1	0.2
A	ga	ss	double	500	0	0.0
A	ga	vs	double	500	8	1.6
A	miy	miy	single	500	3	0.6
A	miy	ss	double	500	0	0.0
A	miy	vs	double	500	0	0.0
A	ss	ss	single	500	6	1.2
A	ss	vs	double	500	0	0.0
A	vs	vs	single	500	11	2.2
A	total	total	single/double	500	123	24.6
study	species1	species2	infection	nymph.tot	nymph.inf	% inf
B	af	af	single	1500	165	11.0
B	af	bav	double	1500	0	0.0
B	af	ga	double	1500	4	0.3
B	af	miy	double	1500	3	0.2
B	af	ss	double	1500	2	0.1
B	af	vs	double	1500	2	0.1
B	bav	bav	single	1500	24	1.6
B	bav	ga	double	1500	0	0.0
B	bav	miy	double	1500	0	0.0
B	bav	ss	double	1500	0	0.0
B	bav	vs	double	1500	4	0.3
B	ga	ga	single	1500	86	5.7
B	ga	miy	double	1500	2	0.1
B	ga	ss	double	1500	0	0.0
B	ga	vs	double	1500	32	2.1
B	miy	miy	single	1500	2	0.1
B	miy	ss	double	1500	2	0.1
B	miy	vs	double	1500	0	0.0
B	ss	ss	single	1500	18	1.2
B	ss	vs	double	1500	1	0.1
B	vs	vs	single	1500	62	4.1
B	total	total	single/double	1500	409	27.3

study	species1	species2	infection	nymph.tot	nymph.inf	% inf
C	af	af	single	2250	265	11.8
C	af	bav	double	2250	0	0.0
C	af	ga	double	2250	5	0.2
C	af	miy	double	2250	5	0.2
C	af	ss	double	2250	11	0.5
C	af	vs	double	2250	5	0.2
C	bav	bav	single	2250	36	1.6
C	bav	ga	double	2250	0	0.0
C	bav	miy	double	2250	0	0.0
C	bav	ss	double	2250	0	0.0
C	bav	vs	double	2250	3	0.1
C	ga	ga	single	2250	95	4.2
C	ga	miy	double	2250	0	0.0
C	ga	ss	double	2250	0	0.0
C	ga	vs	double	2250	35	1.6
C	miy	miy	single	2250	3	0.1
C	miy	ss	double	2250	1	0.0
C	miy	vs	double	2250	0	0.0
C	ss	ss	single	2250	19	0.8
C	ss	vs	double	2250	0	0.0
C	vs	vs	single	2250	69	3.1
C	total	total	single/double	2250	552	24.5

study	species1	species2	infection	nymph.tot	nymph.inf	% inf
D	af	af	single	450	42	9.3
D	af	bav	double	450	0	0.0
D	af	ga	double	450	2	0.4
D	af	miy	double	450	1	0.2
D	af	ss	double	450	3	0.7
D	af	vs	double	450	0	0.0
D	bav	bav	single	450	4	0.9
D	bav	ga	double	450	0	0.0
D	bav	miy	double	450	1	0.2
D	bav	ss	double	450	0	0.0
D	bav	vs	double	450	1	0.2
D	ga	ga	single	450	18	4.0
D	ga	miy	double	450	0	0.0
D	ga	ss	double	450	0	0.0
D	ga	vs	double	450	6	1.3
D	miy	miy	single	450	0	0.0
D	miy	ss	double	450	0	0.0
D	miy	vs	double	450	0	0.0
D	ss	ss	single	450	3	0.7
D	ss	vs	double	450	0	0.0
D	vs	vs	single	450	26	5.8
D	total	total	single/double	450	107	23.8

study	species1	species2	infection	nymph.tot	nymph.inf	% inf
E	af	af	single	900	109	12.1
E	af	bav	double	900	0	0.0
E	af	ga	double	900	0	0.0
E	af	miy	double	900	6	0.7
E	af	ss	double	900	7	0.8
E	af	vs	double	900	0	0.0
E	bav	bav	single	900	5	0.6
E	bav	ga	double	900	0	0.0
E	bav	miy	double	900	0	0.0
E	bav	ss	double	900	0	0.0
E	bav	vs	double	900	0	0.0
E	ga	ga	single	900	20	2.2
E	ga	miy	double	900	0	0.0
E	ga	ss	double	900	0	0.0
E	ga	vs	double	900	6	0.7
E	miy	miy	single	900	0	0.0
E	miy	ss	double	900	0	0.0
E	miy	vs	double	900	0	0.0
E	ss	ss	single	900	12	1.3
E	ss	vs	double	900	0	0.0
E	vs	vs	single	900	23	2.6
E	total	total	single/double	900	188	20.9

study	species1	species2	infection	nymph.tot	nymph.inf	% inf
F	af	af	single	800	80	10.0
F	af	bav	double	800	1	0.1
F	af	ga	double	800	1	0.1
F	af	miy	double	800	2	0.3
F	af	ss	double	800	5	0.6
F	af	vs	double	800	1	0.1
F	bav	bav	single	800	8	1.0
F	bav	ga	double	800	0	0.0
F	bav	miy	double	800	0	0.0
F	bav	ss	double	800	0	0.0
F	bav	vs	double	800	1	0.1
F	ga	ga	single	800	30	3.8
F	ga	miy	double	800	0	0.0
F	ga	ss	double	800	2	0.3
F	ga	vs	double	800	8	1.0
F	miy	miy	single	800	0	0.0
F	miy	ss	double	800	0	0.0
F	miy	vs	double	800	0	0.0
F	ss	ss	single	800	8	1.0
F	ss	vs	double	800	0	0.0
F	vs	vs	single	800	26	3.3
F	total	total	single/double	800	173	21.6

study	species1	species2	infection	nymph.tot	nymph.inf	% inf
G	af	af	single	1000	56	5.6
G	af	bav	double	1000	0	0.0
G	af	ga	double	1000	1	0.1
G	af	miy	double	1000	1	0.1
G	af	ss	double	1000	5	0.5
G	af	vs	double	1000	7	0.7
G	bav	bav	single	1000	9	0.9
G	bav	ga	double	1000	0	0.0
G	bav	miy	double	1000	0	0.0
G	bav	ss	double	1000	0	0.0
G	bav	vs	double	1000	1	0.1
G	ga	ga	single	1000	28	2.8
G	ga	miy	double	1000	0	0.0
G	ga	ss	double	1000	1	0.1
G	ga	vs	double	1000	11	1.1
G	miy	miy	single	1000	0	0.0
G	miy	ss	double	1000	0	0.0
G	miy	vs	double	1000	0	0.0
G	ss	ss	single	1000	13	1.3
G	ss	vs	double	1000	0	0.0
G	vs	vs	single	1000	46	4.6
G	total	total	single/double	1000	179	17.9

study	species1	species2	infection	nymph.tot	nymph.inf	% inf
pooled	af	af	single	7400	788	10.6
pooled	af	bav	double	7400	1	0.0
pooled	af	ga	double	7400	13	0.2
pooled	af	miy	double	7400	20	0.3
pooled	af	ss	double	7400	35	0.5
pooled	af	vs	double	7400	15	0.2
pooled	bav	bav	single	7400	92	1.2
pooled	bav	ga	double	7400	0	0.0
pooled	bav	miy	double	7400	1	0.0
pooled	bav	ss	double	7400	0	0.0
pooled	bav	vs	double	7400	10	0.1
pooled	ga	ga	single	7400	290	3.9
pooled	ga	miy	double	7400	3	0.0
pooled	ga	ss	double	7400	3	0.0
pooled	ga	vs	double	7400	106	1.4
pooled	miy	miy	single	7400	8	0.1
pooled	miy	ss	double	7400	3	0.0
pooled	miy	vs	double	7400	0	0.0
pooled	ss	ss	single	7400	79	1.1
pooled	ss	vs	double	7400	1	0.0
pooled	vs	vs	single	7400	263	3.6
pooled	total	total	single/double	7400	1731	23.4